

Amendments to Claims

Claims 1-2 (Canceled)

Claim 3 (Currently amended): A method for generating a genome-registered collection of reporter gene fusions from an organism comprising the steps of:

- (a) generating a set of gene fusions comprising:
 - 1) a reporter gene or reporter gene complex operably linked to
 - 2) a genomic fragment from an organism of which at least 15% of the genomic nucleotide sequence is known;
- (b) introducing *in vitro* the reporter gene fusions from step (a) into a host organism;
- (c) registering the reporter gene fusions on the basis of sequence homology to the genomic sequence of the organism;
- (d) repeating (a), (b), and/or (c) until reporter gene fusions have been made to at least 15% of the known genomic nucleotide sequence of said organism.

Claim 4 (Original): A method according to Claim 3 wherein the gene fusions of step (a) are generated either *in vivo* or *in vitro*.

Claim 5 (Currently amended): The method of Claim 3 wherein: A method for generating a genome-registered collection of reporter gene fusions comprising:

- (a) said generating a set of gene fusions comprises:
 - 1) generating random nucleic acid fragments from the DNA of an organism of which at least 15% of the nucleotide sequence is known; and
- (b) 2) operably linking the random nucleic acid fragments generated in (1a) to a vector containing a promoterless reporter gene or reporter gene complex in a vector; and
- (c) (b) said registering the reporter gene fusions on the basis of sequence homology to the genomic sequence of the organism of step (c) comprises introducing the vector (b) containing the gene fusions into a host organism;
- (d) determining the nucleic acid sequence of the distal and the proximal ends of the random nucleic acid fragments relative to the reporter gene or reporter gene complex;
- (e) registering the sequenced fusions of step (d) on the basis of sequence homology to the genomic sequence of the host organism;
- (f) repeating (a), (b), and/or (c) until reporter gene fusions have been made to at least 15% of the known genomic nucleotide sequence of said organism

Claim 6 (Currently amended): A method according to Claim 5 wherein the random nucleic acid fragments of step (a) are generated by a method selected from the group consisting of restriction enzyme digestion, physical shearing of the genome and polymerase chain reaction.

Claims 7-8 (Canceled)

Claim 9 (Currently amended): A method according to ~~any one of~~ Claims 1, 3, or ~~5, 7 or 8~~ wherein the organism is selected from the group consisting of prokaryotes and fungi.

Claim 10 (Original): A method according to Claim 9 wherein the prokaryote is an enteric bacterium.

Claim 11 (Original): A method according to Claim 10 wherein the enteric bacterium is selected from the group consisting of *Escherichia* and *Salmonella*.

Claim 12 (Currently amended): A method according to ~~one of~~ Claims 1, 3, or Claim ~~5, 7 or 8~~ wherein the reporter gene or reporter gene complex is selected from the group consisting of *luxCDABE*, *lacZ*, *gfp*, *cat*, *galK*, *inaZ*, *luc*, *luxAB*, *bgaB*, *nptII*, *phoA*, *uidA* and *xyle*.

Claim 13 (Currently amended): A method according to ~~one of~~ Claims 1, 3, or Claim ~~5, 7 or 8~~ wherein at least 50% of the genomic nucleotide sequence is known.

Claims 14-22 (Canceled)